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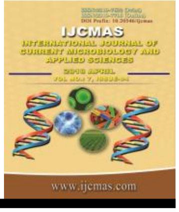

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Correlation and Path Analysis Studies in Advance Lines of Pigeonpea [*Cajanus cajan* (L.) Millspaugh] under Different Environments

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ABSTRACT

An experiment comprising 20 different genotypes of pigeonpea was conducted during *kharif* 2016 in three different environments. In each environment each genotype was sown in a six row plot of four meter length in randomised block design with three replications. Observations were recorded on ten different character viz., days to 50% flowering, days to maturity, plant height (cm), number of primary branches/plant, number of secondary branches/plant, number of pod/plant, number of seed/pod, main shoot length (cm), 100 seed weight (g) and seed yield/plot (g)on five randomly plants of each genotype in each replication. Analysis of variance revealed that significant differences existed among genotypes for all the characters in all the three environments. In general, PCV estimates were higher than the corresponding GCV estimates for all the ten characters in all the three environments. High estimates of broad sense heritability along with high estimates of genetic advance as percent of mean was observed for 100 seed weight in all the three environments. Over all the environments, seed yield per plot is significantly and positively correlated to the days to 50% flowering, days to maturity and number of pods per plants. Days to maturity, number of pods per plant and number of seed per pods not only had direct effect but also positively and significantly associated with seed yield per plot in all the three environments.

Keywords

Pigeonpea, Genetic variability, Heritabiity, Correlation, Path analysis

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Introduction

Pigeonpea [*Cajanus cajan* (L.) Millspaugh] popularly known as arhar or tur is one of the most important pulse crop with diversified uses as food, fodder and fuel. It has been recognized as an important source of dietary protein in the developing countries like India where majority of the population cannot afford to eat non veg foods frequently to fulfil their daily dietary protein requirement. Protein content in commonly grown pigeonpea cultivars ranges between 17.9 to 24.3 g per 100 g for whole grain samples, and between 21.1 to 28.1 g per 100 g in the dal (Salunkhe *et al.*, 1986). Globally, it is cultivated on about 6.23 million hectare area with an annual production of 4.74 million tons with the productivity of 762.4 kg/ha (FAOSTAT, 2015). India has the maximum acreage under pigeonpea, 3.55 million hectare with a total production and productivity of 2.78 million tons and 743 (kg/ha) respectively. This crop is grown in almost all parts of India, however the major states in terms of area and production are Madhya Pradesh, Maharashtra, Rajasthan, Uttar Pradesh, Karnataka, Gujarat and Bihar which together account for 86% of area and 83.8% of national production.

Despite these advantages, the per capita availability of pigeonpea has declined in India mainly due to the widening demand-supply gap caused by mismatch in population and production growth. The major bottlenecks in achieving high productivity include poor crop management and different biotic and abiotic stresses besides the narrow genetic base (Kumar *et al.*, 2004).

The yield is a complex trait which is influenced by a number of components and therefore it is important to find out the direct and indirect contribution of each component trait on seed yield in order to identify important component characters influencing seed yield. The efficacy of any selection programme depends upon the existence and magnitude of available genetic variability for yield and yield contributing traits in the breeding material.

For yield improvement selection of superior parents possessing better heritability and genetic advance for yield contributing traits is an essential prerequisite. Heritability along with genetic advance is more useful than heritability alone in the prediction of resultant effect of selection (Johnson *et al.*, 1955).

It is therefore essential for plant breeder to know the extent of relationship between yield and its various contributing components, which will inevitably, facilitate selection of desirable characteristics. Therefore, the present investigation was undertaken with the objective to find out genetic variability, heritability, expected genetic advance and correlation between different traits and their contribution towards seed yield.

Materials and Methods

The experimental material used in present investigation included17 advance breeding lines of pigeonpea and three checks. All the advance breeding lines along with the three check varieties were grown in a randomized block design (RBD) with three replications in three different environments i.e. Pigeonpea Breeding Block and Pigeonpea Entomology Block at Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar and the third at Agricultural Research Station, Majhera (Almora).Each genotype was sown in a single plot consisted of 6 rows of 4 m length with the 60 cm of inter row and 15 cm of intra row spacing. Recommended agronomic practices and plant protection measures were adopted to raise the uniform crop stand. At each location, observations were recorded on five randomly selected competitive plants from each genotype from each replication on 10 different morphological characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches/plant, number of secondary branches/plant, number of pods/plant, number of seeds/pod, main shoot length (cm), 100 seed weight (g) and seed yield/plot (g).

The mean values computed from the observations for each replication from each location were used for statistical analysis. The Analysis of variance (ANOVA) was done following the method given by Fisher (1920). The phenotypic and genotypic coefficient of variability (PCV, GCV) were computed according to the method suggested by Burton (1952), heritability (h^2) and genetic advance as percent of mean (GA) as suggested by Allard (1960). The correlation coefficients at phenotypic and genotypic levels were estimated from the analysis of variance and covariance as given by Searle (1961). Direct and indirect effects of various characters on seed yield were estimated with the help of path coefficient analysis as suggested by Wright (1921) and Dewey and Lu (1959).

Results and Discussion

Analysis of variance (ANOVA)

The results of analysis of variance for environment I, II and III are presented in (Table 1) and revealed that significant genotypic differences existed for all the characters studied across the environments. In environment I mean squares were significant for all the characters studied except seed yield/plot. In environment II and III significant genotypic variation was present for all traits studied. It is evident from analysis of variance for three different environments that sufficient genetic variability exists among genotypes for all the characters studied and hence desirable improvement can be brought through selection in these different characters. Venkateswarlu (2001), Virdi *et al.,* (2005), Patel and Acharya (2011), Vanisree *et al.,* (2013), Yerimani *et al.,* (2013), Vohra *et al.,* (2015) and Meena *et al.,* (2017) also reported the existence of sufficient genetic variability for these characters in pigeonpea.

PCV, GCV, h^2 and GA

The results on phenotypic (PCV) and genotypic (GCV) coefficients of variability are presented in Table 1. It is clear that, in general, PCV estimates were higher than the corresponding GCV estimates for all the ten characters in all three environments which indicated that these characters were influenced by environment. High estimate of PCV than the corresponding GCV estimates for these characters in pigeonpea were also reported by Basavarajaiah *et al.,* (2000), Gohil (2006), Vange *et al.,* (2009), Mahiboobsa *et al.,* (2012), Rangare *et al.,* (2013), Sharma *et al.,* (2012), Lakhote *et al.,* (2015), Pandey *et al.,* (2015) Vohra *et al.,* (2015) and Meena *et al.,* (2017).

It is clear from the Table 1 that none of the character exhibited high (>20 %) GCV estimates in all the three environments. However, the PCV estimates were high (>20 %) for number of secondary branches / plant, number of pods / plant and seed yield / plot in all the three environments. High estimates of PCV for these three characters indicated that sufficient genetic variability exited in the experimental material and therefore, selection might bring desirable improvement in these characters. Similar kind of results for different characters were also reported by Vange *et al.,* (2009), Mahiboobsa *et al.,* (2012), Singh *et al.,* (2013), Yerimani *et al.,* (2013) and Ajay *et al.,* (2014), Vohra *et al.,* (2015) and Meena *et al.,* (2017).

Higher magnitude of broad sense heritability (>60 %) in all the three environments was observed for days to 50 % flowering, days to maturity and100-seed weight. For rest of the characters the estimates of heritability for all three environments were either moderate or low. Similar kind of results for different characters were also reported by Venkateswarlu (2001), Gohil (2006), Sarsmaker *et al.,* (2008), Mahiboobsa *et al.,* (2012), Rangare *et al.,* (2013), Singh *et al.,* (2013), Ajay *et al.,* (2014), Rao *et al.,* (2015), Vohra *et al.,* (2015) and Meena *et al.,* (2017). For traits like seed yield per plot, main shoot length, plant height, number of primary branches/plant, number of secondary branches/plant, number of pod per plant, main shoot length and number of seeds/pod the estimates of heritability in general were moderate or low which clearly indicated that selection for these characters may not be effective. Similar results for these characters were also reported by Sarsmaker *et al.,* (2008), Shunyu *et al.,* (2013), Ajay *et al.,* (2014), Saroj *et al.,* (2015) and Vohra *et al.,* (2015).

Table.1 Analysis of variance, general mean, range and estimated genetic parameters for 10 quantitative traits in three environments for advance lines of pigeonpea

Source of variation	d.f.	Environ ments	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of secondary branches	No. of pods/ plant	No. of seed/pod	Main shoot length	100 seed weight	Seed yield/ plot
Replications	2	**EI**	0.05	0.65	2101.85**	43.55**	61.11	1254.95*	0.51	384.65*	0.01	426425.61
		EII	5.00**	3.95**	2.21	4.31	17.51	731.27*	0.15	360.81	0.01	28240.41
		EIII	0.517	0.017	1237.56*	2.817	44.51	1602.35	0.61*	171.15	0.016	70080.00
Genotypes	19	**EI**	25.98**	85.10**	1335.618**	7.89*	102.33**	5163.31**	0.75**	257.82**	1.57**	243200.77
		EII	81.52**	140.52**	749.40**	26.99**	90.08**	5916.49**	0.40*	416.14**	1.78**	198330.94**
		EIII	26.15**	85.36**	897.57**	4.697*	34.19*	3802.57**	0.40**	236.71*	1.72**	222104.91*
Error	38	**EI**	0.62	1.45	342.34	3.90	18.81	1062.02	0.20	89.24	0.06	175904.75
		EII	2.38	3.49	30.30	3.66	10.99	170.49	0.22	156.13	0.006	45100.94
		EIII	0.324	0.42	316.05	2.46	15.60	967.84	0.16	110.20	0.05	93992.28
Mean, Range, SEm and Estimated genetic parameters												
Range		**EI**	74.33-86.33	130-147	207.33-288.33	8-13.66	14.33-34.66	144-274.33	3-4.66	74-109	6.25-8.83	1527-2537.33
		EII	71.66-84.33	127.33-146.33	193-262.66	7.33-11.66	14.33-25.33	136-249.33	3.33-4.33	63.33-91.66	6.2-8.63	1320-2233.33
		EIII	69.66-87.00	126.00-149.00	127.66-184.66	6.00-16.33	12-33	62.66-184.33	3-4.33	41.33-80.00	6.46-8.90	540-1481.66
Mean		**EI**	82.35	140.20	245.10	10.75	23.26	219.15	4.00	92.90	7.28	1963.70
		EII	80.38	138.03	221.20	9.58	20.06	203.15	3.81	79.80	7.30	1777.00
		EIII	77.85	137.70	154.76	9.81	18.11	117.76	3.60	56.66	7.60	864.40
PCV %		**EI**	3.65	3.86	10.58	21.27	29.35	22.49	15.10	12.98	10.67	22.67
		EII	3.71	3.88	10.20	18.69	23.26	21.52	12.86	15.46	10.66	20.80
		EIII	6.88	5.09	10.61	34.46	33.73	38.78	14.76	27.49	10.15	35.87
GCV %		**EI**	3.53	3.76	7.42	10.72	22.67	16.87	2.56	8.06	10.17	7.62
		EII	3.65	3.85	6.29	9.00	12.40	15.13	7.44	8.13	10.16	11.62
		EIII	6.59	4.90	10.00	28.40	28.34	37.16	6.93	16.42	10.10	26.14
h^2		**EI**	93.07	95.03	49.16	25.42	59.66	56.28	2.88	38.63	90.47	11.31
		EII	96.37	98.53	38.01	23.17	28.42	49.40	33.45	27.67	90.76	31.24
		EIII	91.70	92.89	88.77	67.95	70.57	91.82	22.05	35.65	98.98	53.10
GA as % of mean		**EI**	7.01	7.56	10.72	11.14	36.08	26.07	0.89	10.33	19.96	5.28
		EII	7.38	7.88	7.99	8.92	13.62	21.90	8.86	8.81	19.94	13.39
		EIII	13.01	9.74	19.41	48.24	49.04	73.35	6.70	20.22	20.70	39.24

***, **: Significant at 5% and 1% probability levels, respectively.**

Table.2 Phenotypic (P) and genotypic (G) correlation coefficients among various characters in pigeonpea genotypes in different environment

Traits	Environ ments		Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of secondary branches	No. of pods /plant	No. of seeds/ pod	Main shoot length	100-Seed weight	Seed yield/plot
Days to 50% flowering	**EI**	**P**	1	0.694**	0.478**	0.115	0.126	0.443**	0.251	0.311*	0.027	0.293*
		G	1	0.734***	0.744**	0.302*	0.196	0.596**	1.441**	0.564**	0.041	1.096*
	EII	**P**	1	0.857**	0.465**	0.549**	0.409**	0.719**	0.418**	0.362**	0.358**	0.583**
		G	1	0.923**	0.529**	0.700**	0.525**	0.762**	0.857**	0.570**	0.379**	0.804**
	EIII	**P**	1	0.639**	0.371**	0.040	0.107	0.297*	0.372**	0.161	0.428**	0.384**
		G	1	0.652**	0.584**	-0.071	0.304*	0.400**	0.605**	0.261*	0.446**	0.653**
Days to maturity	**EI**	**P**		1	0.716	0.118	-0.013	0.483**	0.098	0.091	-0.006	0.392**
		G		1	0.291*	0.202	-0.005	0.625**	0.499**	0.142	-0.005	1.031**
	EII	**P**		1	0.486**	0.627**	0.466**	0.769**	0.435**	0.350**	0.392**	0.649**
		G		1	0.522**	0.776**	0.570**	0.849**	0.947**	0.638**	0.413**	0.915**
	EIII	**P**		1	0.120	0.048	0.037	0.345**	0.515**	0.055	0.354**	0.349**
		G		1	0.202	0.037	0.062	0.456**	0.834**	0.059	0.385**	0.613**
Plant Height	**EI**	**P**			1	0.110	0.157	0.189	0.207	0.501**	0.033	0.461**
		G			1	0.394**	0.452**	0.523**	1.456**	0.546**	-0.061	0.886**
	EII	**P**			1	0.688**	0.392**	0.597**	0.390**	0.321*	0.229*	0.507**
		G			1	0.864**	0.499**	0.677**	0.945**	0.498**	0.242	0.842**
	EIII	**P**			1	0.166	0.071	0.106	0.049	0.266*	0.227	0.174
		G			1	0.118	0.457**	0.514**	0.156	0.057	0.334**	0.681**
Number of primary branches	**EI**	**P**				1	0.219	0.058	0.017	0.089	-0.206	0.093
		G				1	0.381**	0.054	2.721**	-0.022	-0.403**	-0.004
	EII	**P**				1	0.544**	0.723**	0.451**	0.485**	0.314*	0.651**
		G				1	0.610**	0.884**	1.179**	0.822**	0.383**	1.011**
	EIII	**P**				1	-0.094	0.009	0.116	0.038	-0.178	0.044
		G				1	-0.275*	-0.601**	-0.199	-0.549**	-0.357**	-0.140
Number of secondary branches	**EI**	**P**					1	0.340**	0.095	0.116	-0.199	0.188
		G					1	0.614**	0.917	0.275*	-0.347	1.081**
	EII	**P**					1	0.337**	0.371**	0.467**	0.167	0.342**
		G					1	0.419**	0.847**	0.656**	0.197	0.597**

	EIII	**P**					**1**	0.322*	0.075	-0.229	-0.026	0.109
		G					**1**	0.844**	0.265*	-0.128	0.019	1.061**
Number of pods/plant	**EI**	**P**						**1**	-0.022	-0.105	-0.321*	0.479**
		G						**1**	-0.426**	-0.078	-0.336**	1.567**
	EII	**P**						**1**	0.423**	0.275*	0.360**	0.683**
		G						**1**	1.015**	0.512**	0.369**	0.921**
	EIII	**P**						**1**	0.276*	-0.118	0.037	0.479**
		G						**1**	0.360**	-0.247	0.154	1.074**
Number of seeds/pods	**EI**	**P**							**1**	0.279*	0.051	-0.052
		G							**1**	0.685**	0.484**	0.613**
	EII	**P**							**1**	0.326*	0.200	0.574**
		G							**1**	1.099**	0.391**	1.032**
	EIII	**P**							**1**	0.022	0.140	0.312*
		G							**1**	-0.406**	0.302*	0.829**
Main shoot length	**EI**	**P**								**1**	0.214	0.095
		G								**1**	0.338**	-0.159
	EII	**P**								**1**	0.242	0.289*
		G								**1**	0.361**	1.032**
	EIII	**P**								**1**	0.814	-0.013
		G								**1**	0.393**	-0.289*
100-seed weight	**EI**	**P**									**1**	-0.209
		G									**1**	-0.633**
	EII	**P**									**1**	0.314*
		G									**1**	0.436**
	EIII	**P**									**1**	0.107
		G									**1**	0.234
Seed yield /plot	**EI**	**P**										**1**
		G										**1**
	EII	**P**										**1**
		G										**1**
	EIII	**P**										**1**
		G										**1**

*, **: Significant at 5% and 1% probability levels, respectively

Table.3 Path coefficient analysis showing direct and indirect effect of various characters on seed yield/plot at phenotypic level in pigeonpea genotypes in different environment

Traits	Environ ments	Correlation with seed yield/plot	Direct effects		Indirect effects *Via*							
				Days to 50% flowering	Days to maturity	Plant height	No. of primary branches	No. of secondary branches	No. of pods/plant	No of seeds/pod	Main shoot length	100 seed weight (g)
Days to 50% flowering	**EI**	0.293*	-0.377	-	0.286	0.250	-0.001	0.007	0.125	-0.025	-0.010	-0.001
	EII	0.384**	0.207	-	0.019	0.025	-0.001	-0.006	0.114	0.044	-0.004	-0.015
	EIII	0.583**	0.003	-	0.188	0.001	0.154	-0.036	0.160	0.125	-0.018	0.011
Days to maturity	**EI**	0.392**	0.413	-0.233	-	0.092	-0.001	-0.001	0.136	-0.010	-0.003	0.001
	EII	0.349**	0.031	0.132	-	0.008	-0.001	-0.001	0.132	0.061	-0.001	-0.012
	EIII	0.649**	0.221	0.002	-	0.001	0.176	-0.036	0.160	0.130	-0.018	0.011
Plant height (cm)	**EI**	0.461**	0.524	-0.160	0.072	-	0.001	0.009	0.053	-0.021	-0.016	0.002
	EII	0.174	0.069	0.076	0.003	-	-0.001	-0.004	0.040	0.005	-0.008	-0.008
	EIII	0.507**	0.003	0.001	0.107	-	0.193	-0.030	0.124	0.116	-0.016	0.006
Number of primary branches	**EI**	0.093	-0.014	-0.038	0.048	0.057	-	0.013	0.016	-0.001	-0.002	0.013
	EII	0.044	-0.005	0.008	0.001	0.011	-	0.005	0.003	0.0130.0.1 35	-0.001	0.006
	EIII	0.651**	0.282	0.001	0.138	0.002	-	-0.0042	0.151		-0.025	0.008
Number of secondary branches	**EI**	0.188	0.061	-0.042	-0.005	0.082	-0.002	-	0.096	-0.001	-0.003	0.013
	EII	0.109	-0.060	0.022	0.001	0.004	0.001	-	0.123	0.009	0.006	0.001
	EIII	0.342**	-0.078	0.001	0.102	0.001	0.153	-	0.070	0.111	-0.024	0.004
Number of pods/plant	**EI**	0.479**	0.283	-0.149	0.199	0.098	-0.007	0.020	-	0.002	0.003	0.021
	EII	0.479**	0.383	0.061	0.010	0.007	-0.001	-0.019	-	0.033	0.003	-0.001
	EIII	0.683**	0.209	0.002	0.169	0.002	0.203	-0.026	-	0.126	-0.014	0.010
Number of seeds/pod	**EI**	-0.052	0.103	-0.084	0.040	0.108	-0.001	0.005	-0.006	-	-0.009	-0.003
	EII	0.312*	0.120	0.077	0.015	0.003	-0.001	-0.004	0.105	-	-0.001	-0.005
	EIII	0.574**	0.300	0.001	0.095	0.001	0.127	-0.029	0.088	-	-0.017	0.005
Main shoot length	**EI**	0.095	-0.034	-0.104	0.037	0.262	-0.001	0.007	-0.029	-0.028	-	-0.014
	EII	-0.013	-0.030	0.033	0.001	0.018	-0.001	0.013	-0.045	0.002	-	-0.006
	EIII	0.289*	-0.052	0.001	0.077	0.001	0.136	-0.036	0.057	0.097	-	0.006
100 seed weight (g)	**EI**	-0.209	-0.068	-0.009	-0.002	-0.017	0.002	-0.012	-0.090	-0.005	-0.007	-
	EII	0.107	-0.036	0.088	0.010	0.015	0.001	0.001	0.014	0.016	-0.005	-
	EIII	0.314*	0.028	0.001	0.086	0.001	0.088	-0.013	-0.075	0.059	-0.012	-

In all the three environments, high magnitude of genetic advance as percent of mean (>20 %) was observed for number of pods/plant and 100 seed weight which indicated that this character governed by additive gene and therefore to selection based on phenotypic performance is likely to give beneficial results in improving these characters. High heritability does not always indicate high genetic advance. Johnson *et al.,* (1955) suggested that heritability estimates coupled with genetic advance as % of mean together provide a better judgment rather than heritability alone in predicating the resultant effect of selection. In the present study over all the environments, 100 seed weight exhibited high heritability along with almost high genetic advance. This indicated that this character can be improved upon by selection since the character is under control of additive gene effect. For number of pods/plant, the heritability estimates were low to high in different environments coupled with high estimates genetic advance and selection may be helpful in improving this trait because finding reveals that that the character is governed by additive gene effect but the influence of the environment is high. For rest of the characters either the estimate of heritability or of genetic advance was low to moderate and, therefore selection may not be useful in improving these traits as these characters are highly influenced by the environment. Similar kind of result for different traits were also reported earlier by Bhadru (2011), Mahiboobsa *et al.,* (2012), Shunyu *et al.,* (2013), Vanisree *et al.,* (2013), Sharma *et al.,* (2012) and Chethana *et al.,* (2015), Vohra *et al.,* (2015) and Meena *et al.,* (2017).

Correlations and path analysis

In the present study, inter character association under different environments is presented in Table 2. It is evident from tables that in general, the phenotypic and genotypic correlation coefficients were of same sign. However, the magnitudes of genotypic correlation coefficient were higher than the corresponding phenotypic correlation coefficients. Similar kinds of results for different characters were also reported by Sodavadiya *et al.,* (2009), Chandirakala and Subbaraman (2010), Sharma *et al.,* (2012), Singh *et al.,* (2016) and Meena *et al.,* (2017). In the preset study seed yield per plot is significantly and positively correlated to the days to 50% flowering, days to maturity and number of pods per plants under all the three environments. It indicated that an improvement in these positively and significantly correlated traits will bring improvement in the seed yield per plot similar kind of result was also reported earlier by Baskaran and Muthiah (2007), Sodavadiya *et al.,* (2009), Chandirakala and Subbaraman (2010), Sharma *et al.,* (2012), Singh *et al.,* (2016) and Meena *et al.,* (2017). In general the days to 50 % flowering is significantly and positively correlated with the days to maturity, plant height, number of pods per plants and seed yield per plot in all the three environments. In general the days to maturity is significantly and positively correlated with the days to 50% flowering, number of pods per plants and seed yield per plot in all the three environments. Plant height is significantly and positively correlated with days to 50% flowering and main shoot length at phenotypic level in all the three environments. Number of primary branches is non significantly associated with all the characters under study. Number of secondary branches per plant is positively and significantly associated with number of pod per plant in all the three environments. Number of pods per plant exhibited significant and positive association with seed yield per plot in all the three environments. Number of pods per plant and 100 seed weight does not exhibited significant association with any of the characters in all the three environments. Similar kind of observation for correlation between different traits were also reported by Sodavadiya *et al.,* (2009), Chandirakala and Subbaraman (2010), Sharma *et al.,* (2012),Vohra *et al.,* (2015), Singh *et al.*, (2016) and Meena *et al.,* (2017).

A close perusal of Table 3 indicated that days to maturity, number of pods per plant and number of seed per pods not only had direct effect but these characters are also positively and significantly associated with seed yield per plot in all environments. This indicated that there is true correlation between days to maturity, number of pods per plant, number of seed per pods and seed yield per plot and the direct selection through these traits will be rewarding for seed yield improvement. Similar kinds of results were also reported by Shoran (1982), Sarsmaker *et al.,* (2007), Sawant *et al.*, (2009), Sodavadiya *et al.,* (2009), Thanki *et al.*, (2010), Arbad *et al.,* (2014), Vohra *et al.,* (2015) and Meena *et al.,* (2017).

The results on path analysis further indicated that days to 50% flowering not only had high positive direct effect on seed yield per plot it also had high indirect effect via number of pods per plant on seed yield per plot in all the three environments. Results further indicated that though days to 50% flowering had positive and significant correlation with seed yield per plot it exhibited different magnitude of direct effects in different environments. However, days to 50% flowering exhibited high positive indirect effect through number of pods per plant on seed yield per plot. Rest of the characters exhibited very low indirect effect through any of the character on seed yield per plot in the preset study. High indirect effect of days to 50% flowering and days to maturity via number of pods per plant was also reported by Sarsmaker *et al.*, (2007), Arbad *et al.,* (2014), Vohra *et al.,* (2015) and Meena *et al.,* (2017).

The present investigation suggested that sufficient variability existed in experimental material for all the ten characters in all the three environments which offer opportunity for improvement in component traits through selection. High heritability coupled for high genetic advance was observed for 100 seed weight which indicated that selection can be emphasized to improve 100 seed weight. The correlation study revealed that seed yield per plot was significantly and positively correlated to the days to 50% flowering, days to maturity and number of pods per plants under all the three environments which indicated that an improvement in these positively and significantly correlated traits will bring improvement in the seed yield per plot. Path coefficient analysis revealed that days to maturity, number of pods per plant and number seed per pod contributed maximum towards the seed yield per plot.

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